

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:10:43 ; Search time 32.86 Seconds

(without alignments)
136.380 Million cell updates/sec

Title: US-09-331-631A-24_COPY_29_94

Perfect score: 382
Sequence: 1 HDEDDRRGSHSLQCCVQRC.....EQEEDGGRGHWGEGERE 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	382	100.0	637	2 S35221	globulin Bgl1 prec
2	138	36.1	582	2 B53234	vicillin-like stora
3	135	35.3	407	2 T02258	globulin1 - maize
4	133	34.8	540	2 S21825	vicillin-like stora
5	133	34.8	573	2 A53234	globulin-1S, GLBIS
6	129.5	33.9	122	2 C53234	globulin-10 - maize
7	127	33.2	236	2 T01662	globulin-1 - maize
8	93	24.3	509	2 S08059	alpha-globulin typ
9	92	24.1	625	2 A34615	profilaggrin - rat
10	90	23.6	588	1 FWCNMB	alpha-globulin B P
11	85	22.3	639	2 B24810	beta-conglycinin a
12	83.5	21.9	605	2 S06398	alpha-globulin typ
13	76.5	20.0	338	2 S04321	legumin B (clone p
14	76.5	20.0	566	2 T06453	probable Legumin B
15	74.5	19.5	1655	2 T13998	gene mastermind pr
16	73.5	19.2	810	2 T44430	protein FV100 (imp
17	73	19.1	605	1 FMSYBA	beta-conglycinin a
18	73	19.1	605	2 S20707	beta-conglycinin a
19	73	19.1	613	2 S27770	hypothetical prote
20	72	18.8	566	2 S22477	hypothetical prote
21	72	18.8	852	2 A34373	vicillin precursor
22	72	18.6	564	2 S37241	histidine-rich cal
23	71	18.5	185	2 S71512	legumin B - fava b
24	70	18.3	483	2 T06459	hypothetical prote
25	70	18.3	559	2 S52941	6A sucrose-bindin
26	70	18.3	560	2 S52943	period protein (cl
27	70	18.3	1122	2 B26427	period protein (cl
28	70	18.3	1127	2 A25018	period clock prote
29	70	18.3	1130	2 T30251	circadian rhythm p
					repetin - mouse

30	70	18.3	1176	2 C26427	period clock prote
31	70	18.3	1218	2 A26427	period clock prote
32	70	18.3	1218	2 A26588	period clock prote
33	70	18.3	1549	1 A40691	trichohyalin - she
34	69.5	18.2	250	2 B35026	filaggrin B - mus
35	69.5	18.2	255	2 A35026	filaggrin A - mus
36	69.5	18.2	1208	2 S17286	period clock prote
37	69	18.1	558	2 S52951	period protein (cl
38	69	18.1	558	2 S52944	period protein (cl
39	68.5	17.9	654	2 S11049	potassium channel
40	68.5	17.9	654	2 E39113	potassium channel
41	67.5	17.7	254	2 A31488	filaggrin - mouse
42	67.5	17.7	313	2 A28444	filaggrin precurs
43	67.5	17.7	590	2 A40437	glutamic acid-rich
44	67	17.5	228	2 S19132	rb25 protein - ri
45	67	17.5	516	1 FWCNMB	beta-globulin B pr

ALIGNMENTS

Result 1

S35221 globulin Bgl1 precursor - barley

C:Species: Hordeum vulgare (barley)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000

C:Accession: S35221

R:Heck, G.R.; Chamberlain, A.K.; Ho, T.H.D.

Mol. Gen. Genet. 239, 209-218, 1993

A:Title: Barley embryo globulin 1 gene, Bgl1: characterization of cDNA, chromosome ma

A:Reference number: S35221; MUID:93287988

A:Accession: S35221

A:Molecule type: mRNA

A:Residues: 1-637 <HEC>

A:Cross-references: EMBL:M64372; NID:9167003; PIDN:AAA32936.1; PID:9167004

C:Genetics:

A:Gene: Bgl1

A:Map position: 4

C:Superfamily: glycinin

C:Keywords: glycoprotein

P:174-190/Product: globulin Bgl1 #status predicted <MA>

Query Match 100.0%; Score 382; DB 2; Length 637;

Best Local Similarity 100.0%; Pred. No. 1.8e-32;

Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDEDDRRGSHSLQCCVQRCQERPRYSHARCVCEDRDQOQHGHRQEEEDGGRGHWG 60
|||||
Db 29 HDEDDRRGSHSLQCCVQRCQERPRYSHARCVCEDRDQOQHGHRQEEEDGGRGHWG 88

QY 61 EGEREE 66
|||||
Db 89 EGEREE 94

RESULT 2

B53234 vicillin-like storage protein Gb1-L, embryo - maize

N:Alternate names: globulin-1L

C:Species: Zea mays (maize)

C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999

C:Accession: B53234; S21824

R:Belanger, F.C.; Kriz, A.L.

Genetics 129, 863-872, 1991

A:Title: Molecular basis for allelic polymorphism of the maize globulin-1 gene.

A:Reference number: A53234; MUID:92090707

A:Accession: B53234

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-582 <BFL>

A:Cross-references: EMBL:X59083; NID:922283; PIDN:CAA1809.1; PID:922284

A:Experimental source: inbred line W64A6

Query Match 33.9%; Score 129.5; DB 2; Length 122;
Best Local Similarity 37.9%; Pred. No. 7.8e-07;
Matches 22; Conservative 13; Mismatches 18; Indels 5; Gaps 2;

QY 2 DDEDRRGHSLQOCVORCROPRRYSHARCVOECRDQO---OOHGHEDEEGRCG 55
Db 26 DDNHHHGHSKSGCVCVRC-EDRPMHQRPCLCQCEEREKRSRHRHEADRSGE 82

RESULT 7
globulin-1 - maize (fragment)
C:Species: Zea mays (maize)
C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 11-Jan-2000
C:Accession: T01662
R:Hilton, H.; Gaut, B.S.
Genetics 150, 863-872, 1998
A:Title: Speciation and domestication in maize and its wild relatives: evidence from the
A:Reference number: Z14386; MUID:98429537
A:Accession: T01662
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-236 <HLL>
A:Cross-references: EMBL:AF064222; NID:g3414836; PIDN:AC31465.1; PID:g3414837
A:Experimental source: subspecies parviglumis
C:Genetics:
A:Introns: 166/1; 224/3
C:Superfamily: glycinn

Query Match 33.2%; Score 127; DB 2; Length 236;
Best Local Similarity 37.5%; Pred. No. 2.6e-06;
Matches 24; Conservative 14; Mismatches 20; Indels 6; Gaps 3;

QY 2 DDEDRRGHSLQOCVORCROPRRYSHARCVOECRDQOOGHREDEEGRCGHWGE 61
Db 26 DDNHHHGHSKSGCVCVRC-EDRPMHQRPCLCQCEERE--SRHEADRSGE---SSE 79

QY 62 GERE 65
Db 80 DERE 83

RESULT 8
alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)
S08059
N:Alternate names: seed storage protein
C:Species: Gossypium hirsutum (upland cotton)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
C:Accession: S08059
R:Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
A:Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX. Se
A:Reference number: S06398
A:Accession: S08059
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-509 <CHL>
C:Superfamily: glycinn

Query Match 24.3%; Score 93; DB 2; Length 509;
Best Local Similarity 29.4%; Pred. No. 0.018;
Matches 20; Conservative 16; Mismatches 24; Indels 8; Gaps 3;

QY 3 DDEDRRGHSLQOCVORCROPRRYSHARCVOECRDQOOGH---GRHEDEEGRCGRGW 58
Db 33 EDEQOQSOORFOECQCHQOERPERKQOCVRCREKRYOENPMWGEREEAEETE-- 90

QY 59 HGEGEREE 66
Db 91 --EGEEO 96

RESULT 9
A34615
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-Jun-1990 #sequence_revision 09-Oct-1992 #text_change 04-Feb-2000
C:Accession: A34615
R:Haydock, P.V.; Dale, B.A.
DNA Cell Biol. 9, 251-261, 1990
A:Title: Filaggrin, an intermediate filament-associated protein: structural and funct
A:Reference number: A34615; MUID:90274870
A:Accession: A34615
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-625 <HAY>

A:Cross-references: GB:M21759; NID:g204143; PIDN:AAA1161.1; PID:g204144
A>Note: the authors translated the codon GAA for residue 568 as Gln
C:Superfamily: unassigned calmodulin-related proteins; calmodulin repeat homology
C:Keywords: EF hand; epidermis

Query Match 24.1%; Score 92; DB 2; Length 625;
Best Local Similarity 35.1%; Pred. No. 0.028;
Matches 26; Conservative 7; Mismatches 21; Indels 20; Gaps 3;

QY 2 DDEDRRGHSLQOCVORCROPRRYSHARCVOECRDQO-----HGR 45
Db 319 EDESDAQGHQOQOQOOR-QOORQOHE---QEREHQOQPESSQROQSSGRTQRAAR 374

QY 46 HEDEEGRCGRGW 59
Db 375 HEODSDSTRQGRSH 388

RESULT 10
FWCNA
alpha-globulin B precursor (clone C72) - upland cotton
N:Alternate names: seed storage protein; vicilin precursor
C:Species: Gossypium hirsutum (upland cotton)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: A30838; S06911
R:Chlan, C.A.; Pyke, J.B.; Legocki, A.B.; Dure III, L.
Plant Mol. Biol. 7, 475-489, 1986
A:Title: Developmental biochemistry of cottonseed embryogenesis and germination XVIII
A:Reference number: A30838
A:Accession: A30838
A:Molecule type: mRNA
A:Residues: 1-588 <CHL>
A:Cross-references: GB:M16891; NID:g167374; PIDN:AAA33071.1; PID:g167375
A:Experimental source: var. Coker 201
R:Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
A:Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX.
A:Reference number: S06398
A:Accession: S06911
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-81 <CH2>
C:Comment: This is a seed storage protein.
C:Superfamily: glycinn
C:Keywords: glycoprotein; seed; storage protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-588/Product: alpha-globulin storage protein #status predicted <MAT>
F:417/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 23.6%; Score 90; DB 1; Length 588;
Best Local Similarity 31.2%; Pred. No. 0.043;
Matches 20; Conservative 14; Mismatches 28; Indels 2; Gaps 2;

QY 3 DDEDRRGHSLQOCVORCROPRRYSH-ARCVORCROPRRYSH-GRHEDEEGRCGRGW 60
Db 114 EDEQOQSOORFOECQCHQOERPERKQOCVRCREKRYOENPMWGEREEAEETE 173

